



PCT09

## RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/09/926,036

TIME: 10:00:04

Input Set : A:\Sequence

Output Set: N:\CRF3\02132002\I926036.raw

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9 <110> APPLICANT: Rudnicki, Michael A.
11   Sabourin, Luc A.
15 <120> TITLE OF INVENTION: A Caspase Activated Protein Kinase
19 <130> FILE REFERENCE: 12536-2
23 <140> CURRENT APPLICATION NUMBER: US 09/926,036
25 <141> CURRENT FILING DATE: 2000-02-18
29 <150> PRIOR APPLICATION NUMBER: US 60/120,784
31 <151> PRIOR FILING DATE: 1999-02-19
35 <160> NUMBER OF SEQ ID NOS: 11
39 <170> SOFTWARE: PatentIn version 3.1
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58 acagtacgaa cactgtaaga gagacctgaa ccccgaagag ttttgggaga ttattggaga      180
60 actgggcgac ggagccttcg ggaaagtcta taaggcccag aataaagaga ccaatgtttt      240
62 agctgctgca aagggtgattg acaccaaata tgaagaagag cttgaagatt atatggttga      300
64 gattgacata ttagcatctt gtgatcacc aaacatcgctc aagcttctag atgccttcta      360
66 ttacgagaac aaccttttga tctcattga attctgtgca gggggagcag tggatgctgt      420
68 gatgcttgaa cttgagagac cattaactga atcccaaata caagtagtct gcaagcagac      480
70 attagaggca ttgaattact tacatgacaa taaaatcatc caccgagatc taaaagctgg      540
72 caatattctc tttaacctag atggagacat taaattagcg gattttggag tatcagctaa      600
74 aaataccagg acaattcaaa ggagggattc atttattggc acaccatatt ggatggctcc      660
76 tgaagtagtc atgtgtgaga catcaaagga cagaccttat gactacaaag ctgatgtttg      720
78 gtccctgggt attactttta tagaaatggc tgagatagag ccacctcatc atgatgttaa      780
80 tccaatgcgc gtgctgctga aaattgcaaa atctgagccc ccaacattag cacagccatc      840
82 aaaatgggtc tcaaatttta aggactttct aaggaaatgc ttggaaaaga atgtggatgc      900
84 gcggtggacc acgtctcagc tgttgagca tccctttgtt accgttgatt ccaacaaacc      960
86 agtccgagag ttgattgctg aggcacaaggc tgaagtaaca gaagaagttg aagatggcaa      1020
88 ggaagaagat gaggaggagg aagcagagaa tgctctgcca atacctgcaa ataaacgtgc      1080
90 ctcccttgac ctacgattg ccagctctga agaagataaa ctttcacaaa atgcttgat      1140
92 tttggaatct gtgtcagaaa gaacagaaca aagtacttct gaggataaat ttagcaacaa      1200
94 aattcttaata gagaaacctc cgactgacgg tcctgagaag gctgtggatg agcatgcaag      1260
96 tgatgtgaac ttagaaactg gggctgaact aaatgaccaa acagtaggaa tccatgagaa      1320
98 tgggagagag aagaaaagac ccaagctgga aaatctgcca gatacacaag accagcaaac      1380
100 tgtggatgtt aattcagtcg gtgaagaaaa tgagaataat agagtaactt tagaaacgaa      1440
102 cactgattgt ctgaaaccag aggaagacag aaataaagaa aaccaagaga cacttgagag      1500
104 taaacttata caatctgaag aaattaatga cacacatatt caaacaatgg acttagtttc      1560
106 tcaagagact ggagaaaaag aagcagattt tcaggcagtt gacaatgaag ttgggcttac      1620
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| 112 | gctcagtaag  | gcagcacaga  | gtggggaagg  | ggacgaagcc  | ctggcgcccta | cccagacact  | 1800 |
| 114 | agcagagaag  | cccacagagg  | gcccagaggc  | cgggtggggt  | gaggaagagc  | ctcctgggtg  | 1860 |
| 116 | agagagagtt  | gaggataaac  | agccagagca  | gcagcctgca  | gtgtgtgaag  | ctgagggaca  | 1920 |
| 118 | gttaaccagc  | acgtcagaga  | ccacacgggc  | aaccctggag  | caaccggaga  | cggatgaagt  | 1980 |
| 120 | tgagcaggtc  | agcgagtcca  | atagcattga  | ggagctagag  | agacttgtag  | ttactgggtg  | 2040 |
| 122 | tgaggcacgg  | ctctcgggag  | tgaaggtgag  | gcagctgcta  | ctgaggtaga  | tttgagagaga | 2100 |
| 124 | aaagaaaacg  | cacagaaagt  | gcccgttaaa  | gcagagtccc  | aagctcctgc  | agcatcgag   | 2160 |
| 126 | cccagcgagc  | ctcaccctgt  | cttaataccc  | agtattaata  | ttaattctga  | aaccacagaa  | 2220 |
| 128 | aataaagaag  | aatgggtgc   | tttgccaaaa  | cctgaaacca  | tactgccacc  | agagcctgaa  | 2280 |
| 130 | catgaaaagg  | gaaatgacac  | cgactcaggg  | actgggtcca  | ctgtggagaa  | tagcagtggt  | 2340 |
| 132 | gacctgaact  | tgtccatctc  | tagcttcccta | agcaaagcta  | aggacagcgg  | ctcagtgctc  | 2400 |
| 134 | ctgcaggaga  | caagaagaca  | gaagaaaaca  | ttgaagaaaa  | cacgcaagtt  | tattgtcgat  | 2460 |
| 136 | ggtgtagaag  | tgagtgtgac  | gacatcgaag  | atagttacag  | acagcgactc  | caaaacggag  | 2520 |
| 138 | gaactgcgct  | ttctcaggcg  | tcaggaactt  | cgggagctga  | ggcttcttca  | gaaggaggag  | 2580 |
| 140 | cagcgagccc  | agcagcagct  | caatgggaaa  | ctgcagcagc  | agcgggagca  | gatcttcagg  | 2640 |
| 142 | cgttttgagc  | aggagatgct  | gagtaagaag  | cgacaatatg  | accaagaaat  | tgagaattta  | 2700 |
| 144 | gagaagcagc  | agaaacagac  | aattgaacgg  | ctagaacaag  | agcactactaa | ccgcctgaga  | 2760 |
| 146 | gacgaagcca  | agcgcaccaa  | aggagagcag  | gagaaggagc  | tgtccaagtt  | ccagaatgtg  | 2820 |
| 148 | ctgaaaaacc  | gcaagaaggga | ggaacaagaa  | ttgtttcaga  | agcaacaaca  | agagttagat  | 2880 |
| 150 | ggttctctga  | aaaagattat  | ccagcagcag  | aaggcagagt  | tggccaatat  | tgagagagaa  | 2940 |
| 152 | tgctctgaata | acaagcagca  | gctcatgaga  | gctcgagaag  | ccgcaatttg  | ggagcttgaa  | 3000 |
| 154 | gagcgacatt  | tacaagagaa  | gcaccagctg  | cttaaacagc  | agcttaagaa  | tcagtatttc  | 3060 |
| 156 | atgcagagac  | atcagctgct  | aaaacgccat  | gagaaggaaa  | cagaacaaat  | gcagcgctac  | 3120 |
| 158 | aatcaacgac  | ttattgaaga  | actgaaaaac  | agacagactc  | aggaacgagc  | gagactgccc  | 3180 |
| 160 | aagattcaaa  | gaagtgaagc  | caagacacga  | atggccatgt  | ttaaaaaaag  | tttgaggatc  | 3240 |
| 162 | aactcaacag  | ccacaccaga  | ccaggaccgt  | gaaaaaatta  | aacagtttgc  | tgacacaaga  | 3300 |
| 164 | gaaaagagac  | agaaaaatga  | gagaatggct  | cagcatcaaa  | aacatgagag  | ccaaatgcgg  | 3360 |
| 166 | gatcttcagt  | tgcagtgtga  | agccaatgtt  | cgggaactgc  | accagctgca  | gaatgaaaaa  | 3420 |
| 168 | tgccacctgt  | tggttgaaca  | tgagactcag  | aagctgaagg  | agttggatga  | ggagcacagc  | 3480 |
| 170 | caagagctga  | aggagtggag  | agagaagctg  | agaccagga   | agaagacact  | ggaagaagag  | 3540 |
| 172 | tttgccagga  | aactgcagga  | acaggaagtg  | ttctttaaaa  | tgactgggga  | gtccgaatgt  | 3600 |
| 174 | cttaatccat  | cagcacagag  | cggatctctc  | aaattctacc  | ctattcccac  | cttacattcc  | 3660 |
| 176 | actgggtcat  | agcaacagca  | agtgtcctca  | tctggatttg  | gcttctaagt  | acatcattgt  | 3720 |
| 178 | attctcttca  | tcttccacag  | tatgtatgac  | tacaaagaca  | atcacctgct  | tcattctctt  | 3780 |
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| 182 | actaagacag  | atgctcggcc  | atggttggtga | cgtagcatct  | cgtggtaatt  | ccctaagggtg | 3900 |
| 184 | attttgtata  | ttgaccttaa  | atattgtatt  | ctttagacac  | tgttattgaa  | aactgccaga  | 3960 |
| 186 | gacataatgt  | ttaaagttat  | ttggaaaata  | tatctgttac  | atcactaagt  | attaataaat  | 4020 |
| 188 | attgtttttac | ctgatttctc  | aatgatgcta  | aattctatag  | aaaggactct  | gctatagaat  | 4080 |
| 190 | tgggataatt  | ttcttttgta  | aaccaactct  | tacttttaaa  | aagccatgag  | ttagagaata  | 4140 |
| 192 | cgttattgat  | tcagtacata  | gatataat    | tatcactaaa  | caggatcaaa  | atcttttaaa  | 4200 |
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| 198 | atggggcttt  | ccttttggtc  | atgaggaaca  | aagtcccctt  | ctcactgaca  | tcactgtttt  | 4380 |
| 200 | aaaaacttgc  | ttatattacc  | attccgtaga  | aaattacatc  | ctaaaaacaga | tggtgtacaa  | 4440 |
| 202 | agcctgggaa  | gatgggagaa  | ctggctttta  | catgtgagtt  | ggtgagcccc  | tttactctct  | 4500 |
| 204 | gagagatgcc  | cacagctcag  | ggagttctgc  | catcaccgag  | agctcagccc  | tgagctgcag  | 4560 |
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222 gctgagctct atctggttag atggtttaaa aatgcatgtg taattttaat tttataatta 5100
224 ttttgccaag cataattttt tctggacaac cttgtaggta gccttaactt ttagccaact 5160
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248 20 25 30
251 Phe Trp Glu Ile Ile Gly Glu Leu Gly Asp Gly Ala Phe Gly Lys Val
252 35 40 45
255 Tyr Lys Ala Gln Asn Lys Glu Thr Asn Val Leu Ala Ala Ala Lys Val
256 50 55 60
259 Ile Asp Thr Lys Ser Glu Glu Glu Leu Glu Asp Tyr Met Val Glu Ile
260 65 70 75 80
263 Asp Ile Leu Ala Ser Cys Asp His Pro Asn Ile Val Lys Leu Leu Asp
264 85 90 95
267 Ala Phe Tyr Tyr Glu Asn Asn Leu Trp Ile Leu Ile Glu Phe Cys Ala
268 100 105 110
271 Gly Gly Ala Val Asp Ala Val Met Leu Glu Leu Glu Arg Pro Leu Thr
272 115 120 125
275 Glu Ser Gln Ile Gln Val Val Cys Lys Gln Thr Leu Glu Ala Leu Asn
276 130 135 140
279 Tyr Leu His Asp Asn Lys Ile Ile His Arg Asp Leu Lys Ala Gly Asn
280 145 150 155 160
283 Ile Leu Phe Thr Leu Asp Gly Asp Ile Lys Leu Ala Asp Phe Gly Val
284 165 170 175
287 Ser Ala Lys Asn Thr Arg Thr Ile Gln Arg Arg Asp Ser Phe Ile Gly
288 180 185 190
291 Thr Pro Tyr Trp Met Ala Pro Glu Val Val Met Cys Glu Thr Ser Lys
292 195 200 205
295 Asp Arg Pro Tyr Asp Tyr Lys Ala Asp Val Trp Ser Leu Gly Ile Thr
296 210 215 220
299 Leu Ile Glu Met Ala Glu Ile Glu Pro Pro His His Glu Leu Asn Pro
300 225 230 235 240
303 Met Arg Val Leu Leu Lys Ile Ala Lys Ser Glu Pro Pro Thr Leu Ala
304 245 250 255
307 Gln Pro Ser Lys Trp Ser Ser Asn Phe Lys Asp Phe Leu Arg Lys Cys

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315 His Pro Phe Val Thr Val Asp Ser Asn Lys Pro Val Arg Glu Leu Ile
316          290          295          300
319 Ala Glu Ala Lys Ala Glu Val Thr Glu Glu Val Glu Asp Gly Lys Glu
320 305          310          315          320
323 Glu Asp Glu Glu Glu Glu Ala Glu Asn Ala Leu Pro Ile Pro Ala Asn
324          325          330          335
327 Lys Arg Ala Ser Ser Asp Leu Ser Ile Ala Ser Ser Glu Glu Asp Lys
328          340          345          350
331 Leu Ser Gln Asn Ala Cys Ile Leu Glu Ser Val Ser Glu Arg Thr Glu
332          355          360          365
335 Gln Ser Thr Ser Glu Asp Lys Phe Ser Asn Lys Ile Leu Asn Glu Lys
336          370          375          380
339 Pro Thr Thr Asp Gly Pro Glu Lys Ala Val Asp Glu His Ala Ser Asp
340 385          390          395          400
343 Val Asn Leu Glu Thr Gly Ala Glu Leu Asn Asp Gln Thr Val Gly Ile
344          405          410          415
347 His Glu Asn Gly Arg Glu Lys Lys Arg Pro Lys Leu Glu Asn Leu Pro
348          420          425          430
351 Asp Thr Gln Asp Gln Gln Thr Val Asp Val Asn Ser Val Ser Glu Glu
352          435          440          445
355 Asn Glu Asn Asn Arg Val Thr Leu Glu Thr Asn Thr Asp Cys Leu Lys
356          450          455          460
359 Pro Glu Glu Asp Arg Asn Lys Glu Asn Gln Glu Thr Leu Glu Ser Lys
360 465          470          475          480
363 Leu Ile Gln Ser Glu Glu Ile Asn Asp Thr His Ile Gln Thr Met Asp
364          485          490          495
367 Leu Val Ser Gln Glu Thr Gly Glu Lys Glu Ala Asp Phe Gln Ala Val
368          500          505          510
371 Asp Asn Glu Val Gly Leu Thr Lys Glu Glu Thr Gln Glu Lys Leu Gly
372          515          520          525
375 Lys Asp Gly Thr Ala Gln Lys Val Ile Thr Ser Asp Arg Ser Ser Glu
376          530          535          540
379 Val Gly Thr Asp Glu Ala Leu Asp Asp Thr Gln Lys Ala Ala Glu Leu
380 545          550          555          560
383 Ser Lys Ala Ala Gln Ser Gly Glu Gly Asp Glu Ala Leu Ala Pro Thr
384          565          570          575
387 Gln Thr Leu Ala Glu Lys Pro Thr Glu Gly Pro Glu Ala Gly Gly Ala
388          580          585          590
391 Glu Glu Glu Pro Pro Gly Gly Glu Arg Val Glu Asp Lys Gln Pro Glu
392          595          600          605
395 Gln Gln Pro Ala Val Cys Glu Ala Glu Gly Gln Leu Thr Ser Thr Ser
396          610          615          620
399 Glu Thr Thr Arg Ala Thr Leu Glu Gln Pro Glu Thr Asp Glu Val Glu
400 625          630          635          640
403 Gln Val Ser Glu Ser Asn Ser Ile Glu Glu Leu Glu Arg Leu Val Val
404          645          650          655

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407 Thr Gly Ala Glu Ala Arg Ala Leu Gly Ser Glu Gly Glu Ala Ala Ala
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412          675          680          685
415 Lys Ala Glu Ser Gln Ala Pro Ala Ala Ser Gln Pro Ser Glu Pro His
416          690          695          700
419 Pro Val Leu Ile Pro Ser Ile Asn Ile Asn Ser Glu Thr Thr Glu Asn
420 705          710          715          720
423 Lys Glu Glu Met Gly Ala Leu Pro Lys Pro Glu Thr Ile Leu Pro Pro
424          725          730          735
427 Glu Pro Glu His Glu Lys Gly Asn Asp Thr Asp Ser Gly Thr Gly Ser
428          740          745          750
431 Thr Val Glu Asn Ser Ser Gly Asp Leu Asn Leu Ser Ile Ser Ser Phe
432          755          760          765
435 Leu Ser Lys Ala Lys Asp Ser Gly Ser Val Ser Leu Gln Glu Thr Arg
436          770          775          780
439 Arg Gln Lys Lys Thr Leu Lys Lys Thr Arg Lys Phe Ile Val Asp Gly
440 785          790          795          800
443 Val Glu Val Ser Val Thr Thr Ser Lys Ile Val Thr Asp Ser Asp Ser
444          805          810          815
447 Lys Thr Glu Glu Leu Arg Phe Leu Arg Arg Gln Glu Leu Arg Glu Leu
448          820          825          830
451 Arg Leu Leu Gln Lys Glu Glu Gln Arg Ala Gln Gln Gln Leu Asn Gly
452          835          840          845
455 Lys Leu Gln Gln Gln Arg Glu Gln Ile Phe Arg Arg Phe Glu Gln Glu
456          850          855          860
459 Met Leu Ser Lys Lys Arg Gln Tyr Asp Gln Glu Ile Glu Asn Leu Glu
460 865          870          875          880
463 Lys Gln Gln Lys Gln Thr Ile Glu Arg Leu Glu Gln Glu His Thr Asn
464          885          890          895
467 Arg Leu Arg Asp Glu Ala Lys Arg Ile Lys Gly Glu Gln Glu Lys Glu
468          900          905          910
471 Leu Ser Lys Phe Gln Asn Val Leu Lys Asn Arg Lys Lys Glu Glu Gln
472          915          920          925
475 Glu Phe Val Gln Lys Gln Gln Glu Leu Asp Gly Ser Leu Lys Lys
476          930          935          940
479 Ile Ile Gln Gln Gln Lys Ala Glu Leu Ala Asn Ile Glu Arg Glu Cys
480 945          950          955          960
483 Leu Asn Asn Lys Gln Gln Leu Met Arg Ala Arg Glu Ala Ala Ile Trp
484          965          970          975
487 Glu Leu Glu Glu Arg His Leu Gln Glu Lys His Gln Leu Leu Lys Gln
488          980          985          990
491 Gln Leu Lys Asp Gln Tyr Phe Met Gln Arg His Gln Leu Leu Lys Arg
492          995          1000          1005
495 His Glu Lys Glu Thr Glu Gln Met Gln Arg Tyr Asn Gln Arg Leu
496          1010          1015          1020
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